

ABSTRACT

A method for automatic analysis of genomic information in order to determine relationships among genes allows one to determine complex relationships among genes. First a clustering algorithm is chosen and is applied to the table, obtaining sub-tables of data relative to groups of genes that satisfy the chosen clustering criterion. Therefore, all possible combinations of pair of sub-tables are generated and characteristic parameters are calculated for genes contained in these sub-tables. Finally, for each combination a characteristic value is calculated with a decision algorithm defined in function of these parameters, by considering the genes of the combination as constituting a "Gene Network" if this characteristic value exceeds a pre-defined threshold. The method is preferably implemented by a relative system of identification of groups of co-expressed and co-regulated genes comprising an intelligent fuzzy sub-system trained off-line identified by a neural network.